

## Appendix D

```
***** [align] *****  
options = -align -type=protein -matrix=blosum -gapdist=8 -maxdiv=40 -outorder=aligned -gapopen=10 -gapext=0.2 -pwmatrix=blosum -pwgapopen=10 -pwgapext=0.1  
CLUSTAL W (1.83) Multiple Sequence Alignments
```

```
Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: E1-A0209P-2      498 aa
Sequence 2: BAC77020          502 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score:  29
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1:                               Delayed
Sequence:2      Score:2960
Alignment Score 601
```

query.aln  
CLUSTAL W (1.83) multiple sequence alignment

query.dnd  
(E1-A0209P-2:0.35241, BAC77020:0.35241);